

A. Marschel

1631

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/446,415

DATE: 11/16/2000
TIME: 19:13:40

Input Set : A:\11034W01.SEQ.txt
Output Set: N:\CRF3\11162000\I446415.raw

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Plunkett
11/25/00

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: Beamer, Lesa J., Carroll, Stephen F., Eisenber, David
8 (ii) TITLE OF INVENTION: Bactericidal/Permeability-Increasing Protein:
9 Crystallization, X-Ray Diffraction, Three-Dimensional Structure
10 Determination, Rational Drug Design and Molecular Modeling of
11 Related Proteins
13 (iii) NUMBER OF SEQUENCES: 2
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: McAndrews, Held & Malloy
17 (B) STREET: 500 West Madison, 34th Floor
18 (C) CITY: Chicago
19 (D) STATE: Illinois
20 (E) COUNTRY: United States of America
21 (F) ZIP: 60661
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
29 (vi) CURRENT APPLICATION DATA:
C--> 30 (A) APPLICATION NUMBER: US/09/446,415
C--> 31 (B) FILING DATE: 19-Jul-2000
37 (C) CLASSIFICATION:
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER:
36 (B) FILING DATE:
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: McNicholas, Janet M.
41 (B) REGISTRATION NUMBER: 32,918
42 (C) REFERENCE/DOCKET NUMBER: 11034US01;100-248
45 (ix) TELECOMMUNICATION INFORMATION:
46 (A) TELEPHONE: 312/707-8889
47 (B) TELEFAX: 312/707-9155
48 (C) TELEX:
51 (2) INFORMATION FOR SEQ ID NO: 1:
53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH: 1813 base pairs
55 (B) TYPE: nucleic acid
56 (C) STRANDEDNESS: single
57 (D) TOPOLOGY: linear
59 (ii) MOLECULE TYPE: cDNA
62 (ix) FEATURE:
63 (A) NAME/KEY: CDS
64 (B) LOCATTON: 31..1491
66 (ix) FEATURE:
67 (A) NAME/KEY: mat_peptide

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68      (B) LOCATION: 124..1491
70      (ix) FEATURE:
71          (A) NAME/KEY: misc_feature
72          (D) OTHER INFORMATION: "rBPT"
76      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
78      CAGGCCTTGA GGT'TTTGGCA GCTCTGGAGG ATG AGA GAG AAC ATG GCC AGG GUC      54
79                                     Met Arg Glu Asn Met Ala Arg Gly
80                                     -31 -30      -25
82      CCT TGC AAC GCG CCG AGA TGG GTG TCC CTG ATG GTG CTC GTC GCC ATA      102
83      Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile
84                                     -20      -15      -10
86      GGC ACC GCC GTG ACA GCG GCC GTC AAC CCT GGC GTC GTG GTC AGG ATC      150
87      Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile
88                                     -5      1      5
90      TCC CAG AAG GGC CTG GAC TAC GCC AGC CAG CAG GGC ACG GCC GCT CTG      198
91      Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu
92      10      15      20      25
94      CAG AAG GAG CTG AAG AGG ATC AAG ATT CCT GAC TAC TCA GAC AGC TTT      246
95      Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe
96      30      35      40
98      AAG ATC AAG CAT CTT GGG AAG GGG CAT TAT AGC TTC TAC AGC ATG GAC      294
99      Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp
100      45      50      55
102     ATC CGT GAA TTC CAG CTT CCC AGT TCC CAG ATA AGC ATG GTG CCC AAT      342
103     Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn
104      60      65      70
106     GTG GGC CTT AAG TTC TCC ATC AGC AAC GCC AAT ATC AAG ATC AGC GGG      390
107     Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly
108      75      80      85
110     AAA TGG AAG GCA CAA AAG AGA TTC TTA AAA ATG AGC GGC AAT TTT GAC      438
111     Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp
112     90      95      100      105
114     CTG AGC ATA GAA GGC ATG TCC ATT TCG GCT GAT CTG AAG CTG GGC AGT      486
115     Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser
116      110      115      120
118     AAC CCC ACG TCA GGC AAG CCC ACC ATC ACC TGC TCC AGC TGC AGC AGC      534
119     Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser
120      125      130      135
122     CAC ATC AAC AGT GTC CAC GTG CAC ATC TCA AAG AGC AAA GTC GGG TGG      582
123     His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp
124      140      145      150
126     CTG ATC CAA CTC TTC CAC AAA AAA ATT GAG TCT GCG CTT CGA AAC AAG      630
127     Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys
128      155      160      165
130     ATG AAC AGC CAG GTC TGC GAG AAA GTG ACC AAT TCT GTA TCC TCC AAG      678
131     Met Asn Ser Gln Val Cys Glu Lys Val Thr Asn Ser Val Ser Ser Lys
132     170      175      180      185
134     CTG CAA CCT TAT TTC CAG ACT CTG CCA GTA ATG ACC AAA ATA GAT TCT      726
135     Leu Gln Pro Tyr Phe Gln Thr Leu Pro Val Met Thr Lys Ile Asp Ser

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136		190		195		200		
138	GTG	GCT	GGA	ATC	AAC	TAT	GGT	CTG
139	Val	Ala	Gly	Ile	Asn	Tyr	Gly	Leu
140			205				210	
142	GAG	ACC	CTG	GAT	GTA	CAG	ATG	AAG
143	Glu	Thr	Leu	Asp	Val	Gln	Met	Lys
144			220				225	
146	CAC	AAT	CCA	CCT	CCC	TTT	GCT	CCA
147	His	Asn	Pro	Pro	Pro	Phe	Ala	Pro
148			235				240	
150	CAT	GAC	CGC	ATG	GTA	TAC	CTG	GGC
151	His	Asp	Arg	Met	Val	Tyr	Leu	Gly
152	250						255	
154	GCC	GGG	CTT	GTA	TAC	CAA	GAG	GCT
155	Ala	Gly	Leu	Val	Tyr	Gln	Glu	Ala
156							270	
158	GAT	GAC	ATG	ATT	CCA	AAG	GAG	TCC
159	Asp	Asp	Met	Ile	Pro	Lys	Glu	Ser
160							285	
162	TTT	GGA	ACC	TTC	CTA	CCT	GAG	GTG
163	Phe	Gly	Thr	Phe	Leu	Pro	Glu	Val
164							300	
166	ATA	CAG	ATC	CAT	GTC	TCA	GCC	TCC
167	Ile	Gln	Ile	His	Val	Ser	Ala	Ser
168							315	
170	CCC	ACC	GGC	CTT	ACC	TTC	TAC	CCT
171	Pro	Thr	Gly	Leu	Thr	Phe	Tyr	Pro
172	330						335	
174	GTC	CTC	CCC	AAC	TCC	TCC	CTG	GCT
175	Val	Leu	Pro	Asn	Ser	Ser	Leu	Ala
176							350	
178	ACA	ACT	GGT	TCC	ATG	GAG	GTC	AGC
179	Thr	Thr	Gly	Ser	Met	Glu	Val	Ser
180							365	
182	GAG	CTC	AAG	CTG	GAT	AGG	CTG	CTC
183	Glu	Leu	Lys	Leu	Asp	Arg	Leu	Leu
184							380	
186	GGC	CCC	TTC	CCG	GTT	GAA	TTG	CTG
187	Gly	Pro	Phe	Pro	Val	Glu	Leu	Gln
188							395	
190	CCC	ATT	CTT	GTG	CTG	CCC	AGG	GTT
191	Pro	Ile	Leu	Val	Leu	Pro	Arg	Val
192	410						415	
194	CCT	CTC	CCG	ACG	CCG	GCC	AGA	GTC
195	Pro	Leu	Pro	Thr	Pro	Ala	Arg	Val
196							430	
198	CCT	CAC	CAG	AAC	TTC	CTG	CTG	TTC
199	Pro	His	Gln	Asn	Phe	Leu	Leu	Phe
200							445	

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202 TGAAGGCACC AGGGGTGCCC GGGGCTGTCA GCCGCACCTG TTCCTGATGG GCTGTGGGGC 1551
204 ACCGGCTGCC TTTCCTCAGG GAATCCTCTC CAGATCTTAA CCAAGAGCCC CTTCCAAAC 1611
206 TCTTCGAETC AGATTTCAGAA ATGATCTAAA CACGAGGAAA CATTATTCAT TGGAAAAGTG 1671
208 CATCGTGTGT ATTTTAGGGA TTAATGAGCTT CTTTCAAGGG CTAAGGCTGC AGAGATATTT 1731
210 CTPCCAGGAA TCGTGTTCAT ATTGTAACCA AGAAATTTCC ATTGTGCTT CATGAAAAAA 1791
212 AACTTCTGGT TTTTTCATG TG 1813
215 (2) INFORMATION FOR SEQ ID NO: 2:
217 (i) SEQUENCE CHARACTERISTICS:
218 (A) LENGTH: 487 amino acids
219 (B) TYPE: amino acid
220 (D) TOPOLOGY: linear
222 (ii) MOLECULE TYPE: protein
224 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
226 Met Arg Glu Asn Met Ala Arg Gly Pro Cys Asn Ala Pro Arg Trp Val
227 -31 -30 -25 -20
229 Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val
230 -15 -10 -5 1
232 Asn Pro Gly Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala
233 5 10 15
235 Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys
236 20 25 30
238 Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly
239 35 40 45
241 His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser
242 50 55 60 65
244 Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser
245 70 75 80
247 Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe
248 85 90 95
250 Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile
251 100 105 110
253 Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr
254 115 120 125
256 Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His
257 130 135 140 145
259 Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
260 150 155 160
262 Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys
263 165 170 175
265 Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu
266 180 185 190
268 Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu
269 195 200 205
271 Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys
272 210 215 220 225
274 Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro
275 230 235 240
277 Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly
278 245 250 255

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280 Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala
281          260          265          270
283 Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser
284          275          280          285
286 Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val
287 290          295          300          305
289 Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
290          310          315          320
292 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
293          325          330          335
295 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
296          340          345          350
298 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
299          355          360          365
301 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
302 370          375          380          385
304 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
305          390          395          400
307 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
308          405          410          415
310 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val
311          420          425          430
313 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe
314          435          440          445
316 Gly Ala Asp Val Val Tyr Lys
317 450          455

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VERIFICATION SUMMARY DATE: 11/16/2000
PATENT APPLICATION: US/09/446,415 TIME: 19:13:41

Input Set : A:\11034W01.SEQ.txt
Output Set: N:\CRF3\11162000\I446415.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]